



S3 Fig. Differential expression analysis of P-BE and nonP-BE microarray data highlighted more than 700 genes potentially involved in BE malignant progression. A. Heatmap of genes filtered after differential expression analysis with a conservative cutoff ($Lods \geq 5$). Each dataset is represented with a different colour in the bottom coloured side bar

and each BE progression group is represented by the upper coloured bar (black and grey). **B.** Top 20 GO Biological Processes ($q\text{-value} < 0.05$) over-represented among significantly up-regulated (left plot, in red) and down-regulated (right plot, in blue) genes. Yellow dots illustrate the adjusted Ps for each GO category.